# *B3galnt2* Cas9-CKO Strategy


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**Reviewer:** Xueting Zhang


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# Project Overview

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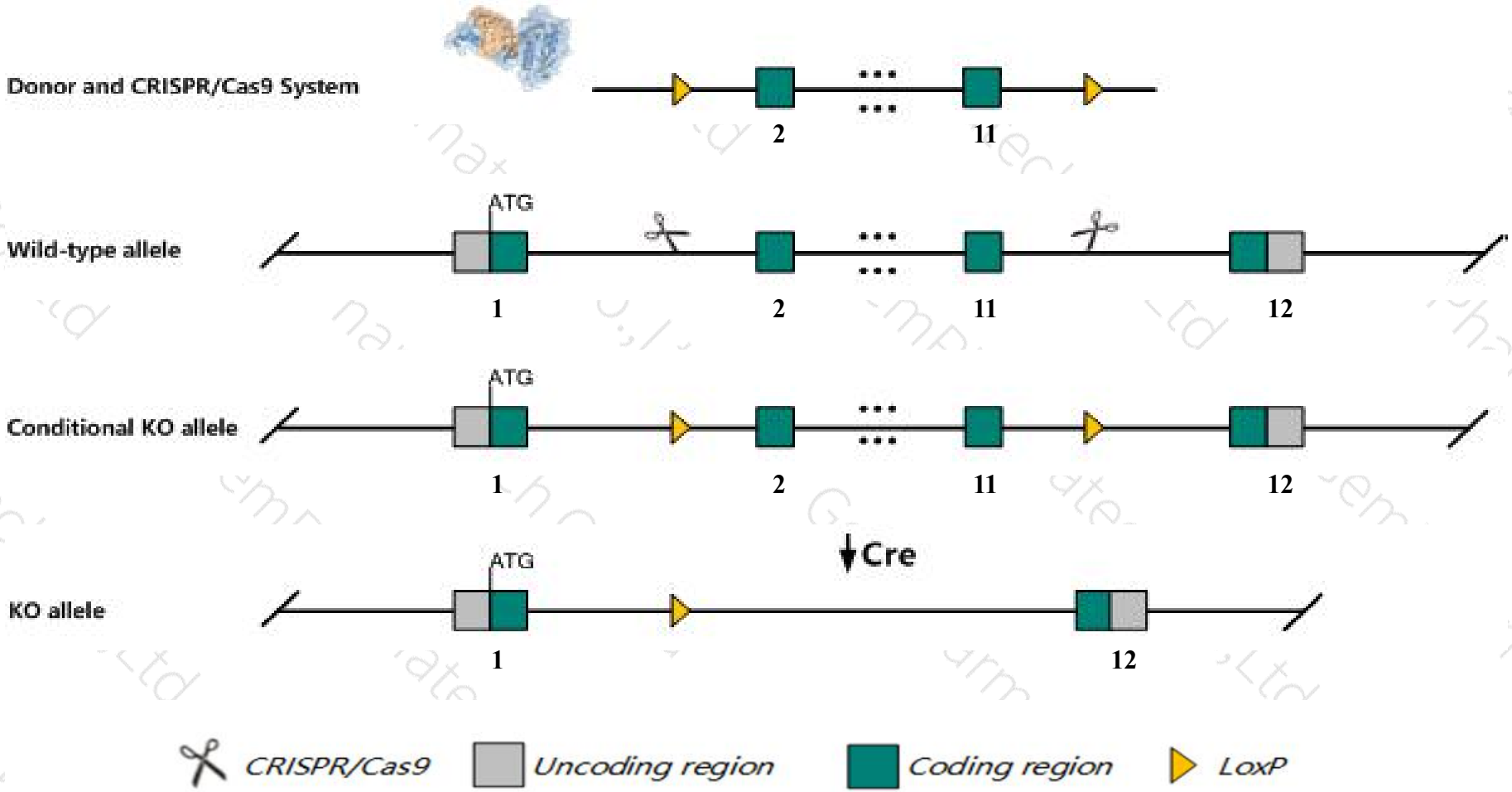
|---|---|
| **Project Name** | ***B3galnt2*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *B3galnt2* gene. The schematic diagram is as follows:



# Technical routes

- The *B3galnt2* gene has 12 transcripts. According to the structure of *B3galnt2* gene, exon2-exon11 of *B3galnt2-201* (ENSMUST00000099747.4) transcript is recommended as the knockout region.The region contains 1259bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *B3galnt2* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

# Notice

- The effect of transcripts 202,205,209 is unknown.
- *Gm18856* gene may be destroyed.
- The *B3galnt2* gene is located on the Chr13. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

# Gene information （NCBI）

集萃药康 GemPharmatech

## B3galnt2 UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2 [Mus musculus (house mouse)]

Gene ID: 97884, updated on 13-Mar-2020

### Summary

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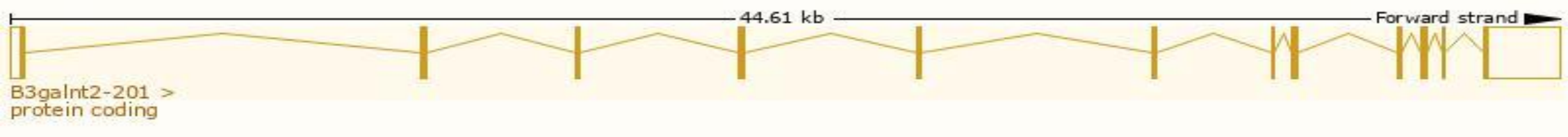
|---|---|
| **Official Symbol** | B3galnt2 provided by MGI |
| **Official Full Name** | UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2 provided by MGI |
| **Primary source** | MGI:MGI:2145517 |
| **See related** | Ensembl:ENSMUSG00000039242 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | A930105D20Rik, C80633, D230016N13Rik |
| **Expression** | Ubiquitous expression in bladder adult (RPKM 13.6), CNS E11.5 (RPKM 13.0) and 28 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

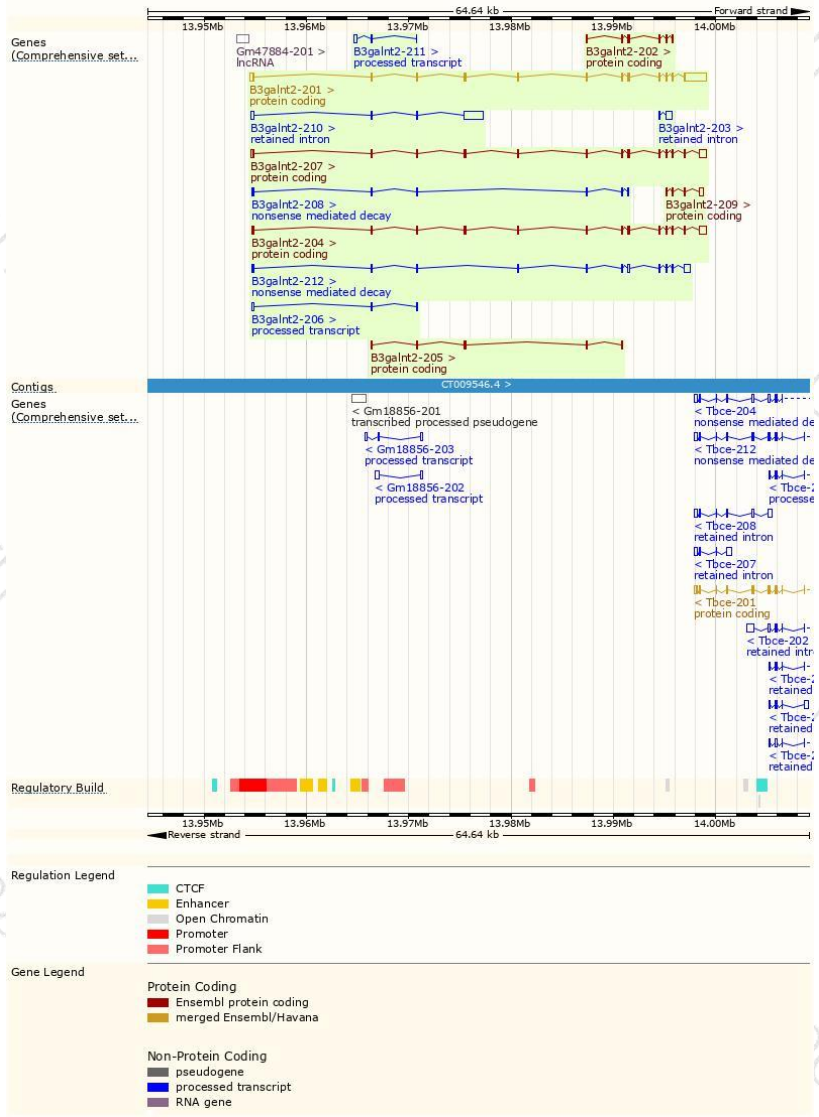
The gene has 12 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| B3galnt2-201 | ENSMUST00000099747.4 | 3892 | 504aa | Protein coding | CCDS26246 | Q8BG28 | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| B3galnt2-207 | ENSMUST00000221974.1 | 2439 | 504aa | Protein coding | CCDS26246 | Q8BG28 | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| B3galnt2-204 | ENSMUST00000221300.1 | 2397 | 504aa | Protein coding | CCDS26246 | Q8BG28 | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| B3galnt2-202 | ENSMUST00000220681.1 | 767 | 251aa | Protein coding | - | A0A1Y7VLK8 | CDS 5' incomplete TSL:3 |
| B3galnt2-209 | ENSMUST00000222420.1 | 693 | 124aa | Protein coding | - | A0A1Y7VK56 | CDS 5' incomplete TSL:3 |
| B3galnt2-205 | ENSMUST00000221333.1 | 602 | 201aa | Protein coding | - | A0A1Y7VLV9 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 |
| B3galnt2-212 | ENSMUST00000223483.1 | 1876 | 143aa | Nonsense mediated decay | - | A0A1Y7VJJ6 | TSL:1 |
| B3galnt2-208 | ENSMUST00000222110.1 | 795 | 123aa | Nonsense mediated decay | - | A0A1Y7VLZ2 | TSL:5 |
| B3galnt2-206 | ENSMUST00000221764.1 | 435 | No protein | Processed transcript | - | - | TSL:3 |
| B3galnt2-211 | ENSMUST00000223389.1 | 434 | No protein | Processed transcript | - | - | TSL:5 |
| B3galnt2-210 | ENSMUST00000223307.1 | 2400 | No protein | Retained intron | - | - | TSL:1 |
| B3galnt2-203 | ENSMUST00000220932.1 | 751 | No protein | Retained intron | - | - | TSL:2 |

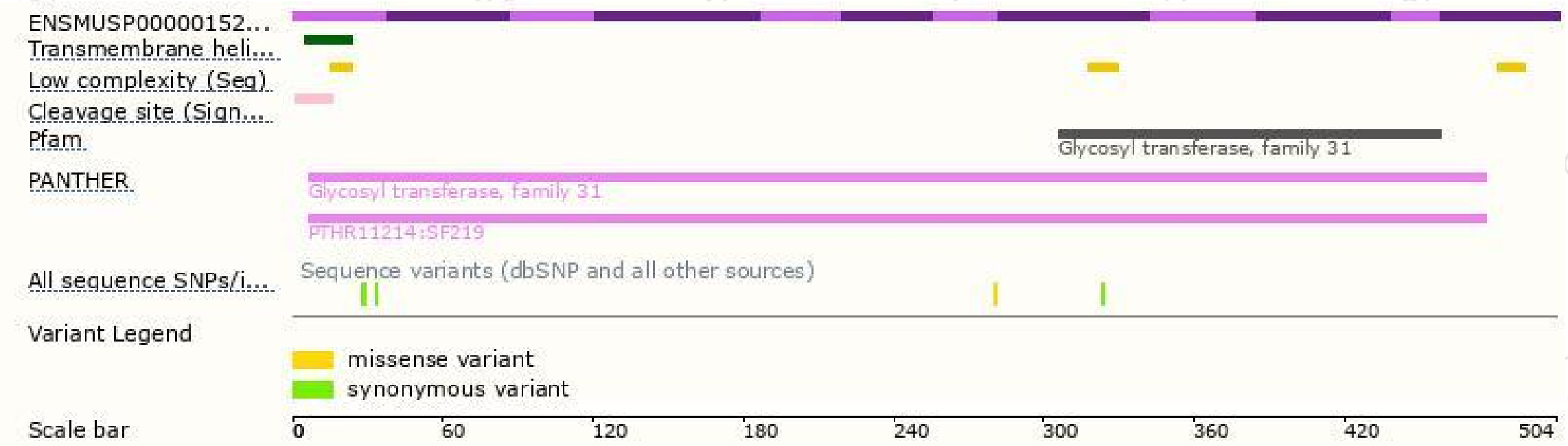
The strategy is based on the design of *B3galnt2-201* transcript,The transcription is shown below



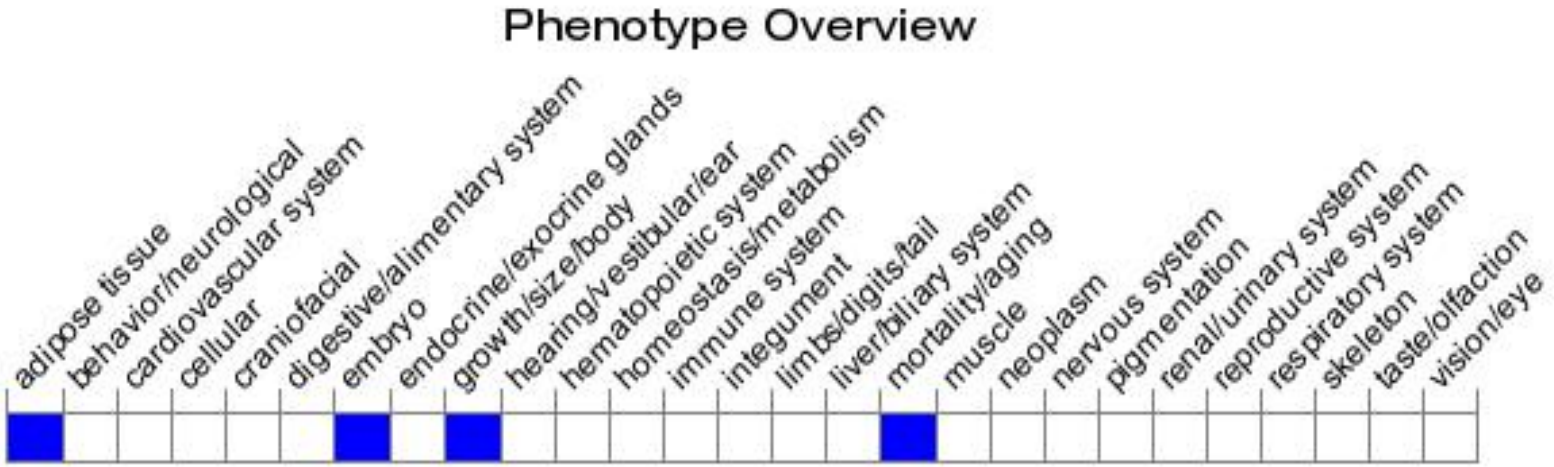
# Genomic location distribution



# Protein domain



# Mouse phenotype description(MGI )




*Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).*

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If you have any questions, you are welcome to inquire.

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